## **RAW SEQUENCE LISTING**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/574.902
Source:	IFWP
Date Processed by STIC:	4/26/06

## ENTERED



**IFWP** 

RAW SEQUENCE LISTING DATE: 04/26/2006
PATENT APPLICATION: US/10/574,902 TIME: 07:34:04

Input Set : F:\Final Sequence List-13987-00003-US.txt

Output Set: N:\CRF4\04262006\J574902.raw

```
3 <110> APPLICANT: Cirpus, Petra
             Oswald, Oliver
             Lerchl, Jens
      5
             Martin, William Frank
             Hoffmeister, Meike
      9 <120> TITLE OF INVENTION: Trans-2-enoyl-CoA reductase gene of Euglena gracilis
     11 <130> FILE REFERENCE: 13987-00003-US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/574,902
C--> 13 <141> CURRENT FILING DATE: 2006-04-07
     13 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/011294
     14 <151> PRIOR FILING DATE: 2004-10-08
     16 <150> PRIOR APPLICATION NUMBER: EP 03022783.9
     17 <151> PRIOR FILING DATE: 2003-10-10
     19 <150> PRIOR APPLICATION NUMBER: EP 04007051.8
    20 <151> PRIOR FILING DATE: 2004-03-24
     22 <160> NUMBER OF SEQ ID NOS: 55
     24 <170> SOFTWARE: PatentIn version 3.3
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     28 <211> LENGTH: 1620
     29 <212> TYPE: DNA
     30 <213> ORGANISM: Euglena gracilis
     32 <220> FEATURE:
     33 <221> NAME/KEY: CDS
     34 <222> LOCATION: (1)..(1620)
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     39 1
                        5
     41 ctc tgc ctg tgc gtg gca acg gta ttg ttg gcg act gga tcc aac ccc
                                                                               96
     42 Leu Cys Leu Cys Val Ala Thr Val Leu Leu Ala Thr Gly Ser Asn Pro
                                                                              144
     45 acc qcc ctq tcc act qct tcc act cqc tct ccq acc tca ctq gtc cqt
     46 Thr Ala Leu Ser Thr Ala Ser Thr Arg Ser Pro Thr Ser Leu Val Arg
     47
                35
                                    40
                                                                              192
     49 ggg gtg gac agg ggc ttg atg agg cca acc act gca gcg gct ctg acg
     50 Gly Val Asp Arg Gly Leu Met Arg Pro Thr Thr Ala Ala Ala Leu Thr
     53 aca atg aga gag gtg ccc cag atg gct gag gga ttt tca ggc gaa gcc
                                                                              240
     54 Thr Met Arg Glu Val Pro Gln Met Ala Glu Gly Phe Ser Gly Glu Ala
                            70
                                                                              288
     57 acg tet gea tgg gee gee geg ggg eeg cag tgg geg geg eeg ete gtg
     58 Thr Ser Ala Trp Ala Ala Ala Gly Pro Gln Trp Ala Ala Pro Leu Val
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Input Set : F:\Final Sequence List-13987-00003-US.txt

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3 100 105 110	
5 agc gtg cgg cgg ccg ctg gca gcg ctg gcg gag ctg ccc acc gcg gtc	384
6 Ser Val Arg Arg Pro Leu Ala Ala Leu Ala Glu Leu Pro Thr Ala Val	
7 115 120 125	
9 acc cac ctg gcc ccc ccg atg gcg atg ttc acc acc aca gcg aag gtc	432
O Thr His Leu Ala Pro Pro Met Ala Met Phe Thr Thr Ala Lys Val	
1 130 135 140	
3 atc cag ccc aag att cgt ggc ttc atc tgc acg acc acc cac ccg atc	480
4 Ile Gln Pro Lys Ile Arg Gly Phe Ile Cys Thr Thr Thr His Pro Ile	
5 145 150 155 160	
7 ggc tgt gag aag cgg gtc cag gag gag atc gcg tac gcc cgt gcc cac	528
8 Gly Cys Glu Lys Arg Val Gln Glu Glu Ile Ala Tyr Ala Arg Ala His	
9 165 170 175	
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2 Pro Pro Thr Ser Pro Gly Pro Lys Arg Val Leu Val Ile Gly Cys Ser	
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6 Thr Gly Tyr Gly Leu Ser Thr Arg Ile Thr Ala Ala Phe Gly Tyr Gln	
7 195 200 205	
9 gcc gcc acg ctg ggc gtg ttc ctg gcg ggc ccc ccg acg aag ggc cgc	672
O Ala Ala Thr Leu Gly Val Phe Leu Ala Gly Pro Pro Thr Lys Gly Arg	
1 210 215 220	
3 ccc gcc gcg gcg ggc tgg tac aac acc gtg gcg ttc gag aag gcc gcc	720
4 Pro Ala Ala Ala Gly Trp Tyr Asn Thr Val Ala Phe Glu Lys Ala Ala	
5 225 230 235 240	
7 ctg gag gcc ggg ctg tac gcc cgg agc ctt aat ggc gac gcc ttc gac	768
8 Leu Glu Ala Gly Leu Tyr Ala Arg Ser Leu Asn Gly Asp Ala Phe Asp	
9 245 250 255	
9 245 250 255 01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc	816
	816
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc	816
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly	816 864
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03 260 265 270	
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03 260 265 270 05 acg gtg gac ctc gtg gtg tac agc atc gcc gcc ccg aag cgg acg gac	
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03 260 265 270 05 acg gtg gac ctc gtg gtg tac agc atc gcc gcc ccg aag cgg acc gac 06 Thr Val Asp Leu Val Val Tyr Ser Ile Ala Ala Pro Lys Arg Thr Asp	
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03 260 265 270 05 acg gtg gac ctc gtg gtg tac agc atc gcc gcc ccg aag cgg acg gac 06 Thr Val Asp Leu Val Val Tyr Ser Ile Ala Ala Pro Lys Arg Thr Asp 07 275 280 285	864
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03 260 265 270 05 acg gtg gac ctc gtg gtg tac agc atc gcc gcc ccg aag cgg acg gac 06 Thr Val Asp Leu Val Val Tyr Ser Ile Ala Ala Pro Lys Arg Thr Asp 07 275 280 285 09 cct gcc acc ggc gtc ctc cac aag gcc tgc ctg aag ccc atc ggc gcc	864
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	864
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	864 912
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	864 912
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	864 912
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	912 960
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	912 960
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	912 960
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	912 960 1008
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	912 960 1008
01 tcc aca acg aag gcg cgg acg gtc gag gcg atc aag cgg gac ctc ggc 02 Ser Thr Thr Lys Ala Arg Thr Val Glu Ala Ile Lys Arg Asp Leu Gly 03	912 960 1008

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						tgg											1152
	Gly		Glu	Met	Thr	Trp		Val	Tyr	Trp	Ser		Thr	Ile	Gly	Glu	
131		370					375					380					1000
	_	_	_	_		gag	_	_	-	_	_		_	_			1200
	385	гуѕ	ьуѕ	Asp	vai	Glu 390	гуѕ	Ala	Ата	ьуѕ	395	ire	1111	GIII	GIII	400	
		tac	cca	aca	tac	ccd	ata	ata	acc	aag		tta	atc	acc	cag		1248
						Pro											1210
139	<b>U</b> -1	072			405					410					415		
	aqc	tcc	gcc	atc	ccq	gtg	qtq	ccq	ctc	tac	atc	tgc	ctg	ctg	tac	cgc	1296
						Val											
143				420					425	_		_		430			
145	gtt	atg	aag	gag	aag	ggc	acc	cac	gag	ggc	tgc	atc	gag	cag	atg	gtg	1344
146	Val	Met	_	Glu	Lys	Gly	Thr		Glu	Gly	Cys	Ile		Gln	Met	Val	
147			435					440					445				
		_			_	aag	_						-			_	1392
	Arg		Leu	Inr	Thr	Lys		Tyr	Pro	Glu	Asn		Ala	Pro	тте	vaı	
151	ant.	450	~~~	<b>~~</b>	aat	ata	455	a+a	ant.	<b>~</b> 3~	taa	460	ata	aca	a a a	aat	1440
						gtg Val											1440
	465	Gra	ALG	Ory	nr 9	470	nr 9	vai	пор	лор	475	Olu	1100	1114	01.0	480	
		caq	caq	act	att	aag	qac	ctc	taa	agc		ata	agc	act	qcc		1488
		_	_	_	-	Lys	_			_	-	-	-				
159					485	-	_		_	490					495		
161	ctc	aag	gac	atc	tcc	gac	ttc	gct	ggg	tat	caa	act	gag	ttc	ctg	cgg	1536
162	Leu	Lys	Asp	Ile	Ser	Asp	Phe	Ala	Gly	Tyr	Gln	Thr	Glu	Phe	Leu	Arg	
163				500					505					510			
						att											1584
	ьeu	Pne	G1y 515	Pne	GIY	Ile	Asp	_	vaı	Asp	Tyr	Asp	525	Pro	vaı	Asp	
167	ata	asa		asa	ata	ccc	act	520	acc	cac	cad	tag	323				1620
	_		_	_		Pro	_		_	_	_	cag					1020
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			EQUE														
		Ser	Cys	Pro	Ala	Ser	Pro	Ser	Ala	Ala	Val	Val	Ser	Ala	Gly	Ala	
183					5		_	_		10				_	15	_	
	Leu	Cys	Leu	_	val	Ala	Thr	Val		Leu	Ala	Thr	GLY		Asn	Pro	
187	π <b>.</b> ~	~ רא	T 0	20	Th∽	<b>π1</b> -	e.~	mh~	25	C~~	Dro	Th~	C0~	30	t/⊃1	7~~	
190	inr	AIG	ьеи 35	ser	Inr	Ala	ser	40	Arg	ser	<b>PIO</b>	TIIT	45	ьeu	val	ALG	
	Glv	Val		Ara	Glv	Leu	Met		Pro	Thr	Thr	Ala		Ala	Len	Thr	
195	O+ 3	50	p	9	y	u	55	******				60			u		
	Thr		Ara	Glu	Val	Pro		Met	Ala	Glu	Glv		Ser	Gly	Glu	Ala	
			ر								4			4			

Input Set : F:\Final Sequence List-13987-00003-US.txt
Output Set: N:\CRF4\04262006\J574902.raw

202	100	<i>6</i> E					70					75					80
203			Cor	ת דת	Trn	ת דת		ת ז ת	C117	Dro	Cln		ת 1 ת	ר [ ת	Dro	T 011	
206   Ala   Ala   Ala   Ser   Ser   Ala   Leu   Ala   Leu   Trp   Trp   Trp   Ala   Ala   Arg   Arg		1111	ser	на	пр		нта	ніа	Gry	PIO		тър	нта	нта	PIO		vaı
100   105   116   116   117   118   119   119   120		77.	77.	77.	C 0 20		71.	T 011	71.	т от		Пии	Пии	7.7.	71.		7~~
Ser Val Arg Arg Arg Pro Leu Ala Ala Leu Ala Glu Leu Pro Thr Ala Val		Ala	Ala	Ala		ser	Ala	ьeu	Ата		пр	пр	пр	Ala		Arg	Arg
115		a	**- 7	7		D	<b>T</b>	<b>7</b> . 1	77.		<b>7</b> .7_	<b>~</b> 1	<b>7</b>	D		7.7	77-7
The His Leu Ala Pro Pro Met Ala Met Phe The The The Ala Lys Val		ser	vaı	_	Arg	Pro	Leu	Ala		ьeu	Ala	GIU	Leu		Thr	Ата	vai
136		ml	TT 2 -		7 T -	D	D	M - 4-		M-L	Dla a	mla sa	ml		7.7.	T	7747
116		Thr		ьeu	Ата	Pro	Pro		Ата	мет	Pne	THE		THE	Ala	ьys	vai
145		<b>-</b> 3 -		D	*	<b>71</b> -	7		Dl	~1.	<b>a</b>	ml		m1	77.2 -	D	T1 -
See See See See See See See See See Se			GIII	PIO	ьуѕ	тте	_	Gry	Pne	тте	Cys		IIII	1111	HIS	PIO	
165			O	a1	T	7		a1	a1	<b>~1</b>	T1.		m	<b>71</b>	7	7.7.	
Pro   Pro   Pro   Pro   Pro   Ser   Pro   Gly   Pro   Lys   Lys   Reg   Val   Leu   Val   Ile   Gly   Cys   Ser   190		GIA	Cys	GIU	ьуѕ	_	vai	GIII	GIU	GIU		Ala	ıyı	Ala	Arg		HIS
180		Dece	Dage	mbaa	C		<b>~1</b>	Deca	T	71		т	7707	Tl.	~1··		Com
Second   S		Pro	Pro	THE		Pro	GIY	Pro	ьys		vaı	Leu	vai	тте		Cys	ser
195		mb	<b>~1</b>			T	0	III la sa	7		mb so	77.	ח ח ת	Dha		Пт тъс	C1 ~
234   Ala   Ala   Ala   Thr   Leu   Gly   Val   Phe   Leu   Ala   Gly   Pro   Pro   Thr   Lys   Gly   Arg   215   210   220		THE	GIY	_	GIY	ьeu	ser	THE	_	тте	THE	Ата	Ala		GTĀ	ıyı	GIII
235		77.	77.		T	<u>ما</u>	77- T	Db.		77.	a1	Desc	Dwa		T	~1	7
238   Pro   Ala   Ala   Ala   Ala   Ala   Ala   Ala   Ala   Cly   Trp   Trp   Asn   Trp   Val   Ala   Ala   Ala   Cly   Ala   Ala		Ата		THE	ьeu	GIY	vaı		ьeu	Ата	GIY	PIO		1111	ьуѕ	GIY	Arg
239		Dro		77.	77.	C1	m		7 0 0	mb~	7727	ת ז ת		C1.,	T	ת 1 ת	77.
242   Leu Glu Ala Gly Leu Tyr Ala Arg Ser Leu Asn Gly Asp Ala Phe Asp   245   255   256   255   256   255   256   255   256   255   256   255   256   255   256   255   256   255   256   257   250   255   256   257   250   255   256   257   250   255   250   250   250   250   250   250   250   250   250   255   250   250   255   255   250   255   255   250   255   255   250   255   255   250   255   255   250   255   255   250   255   255   255   250   255   255   255   250   255			Ald	Ald	Ald	Gry	_	ıyı	ASII	1111	vaı		Pile	GIU	пåр	ALA	
243			C1.,	777	C1	T 011		ר [ ת	71 ***	Cor	T 011		C1.,	7 cn	ת 1 ת	Dho	
246   Ser Thr Thr Lys		ьец	GIU	Ата	СТУ		ıyı	Ата	Arg	ser		ASII	Gry	Asp	мта		ASP
247       260       Val       Val       Tyr       Ser       Ile       Ala       Pro       Lys       Arg       Thr       Asp       Leu       Val       Val       Tyr       Ser       Ile       Ala       Ala       Pro       Lys       Arg       Thr       Asp         251       275       275       280       280       285       285       285         254       Pro       Ala       Thr       Gly       Val       Leu       His       Lys       Ala       Cys       Leu       Lys       Pro       Ile       Gly       Ala         255       290       295       300       3		Cor	Thr	Thx	T 1.00		720	Th∝	77-7	C111		Tla	Tvc	7~~	7) cm		Clu
Second No.   Sec		ser	1111	1111	-	MIA	Arg	IIII	vaı		Ala	116	цуѕ	Arg	_	Leu	GIY
251       275       280       285       285       296       11e Gly Ala       Ala Cys Leu Lys Pro Ile Gly Ala       255       290       295       295       300		Thr	t/al	λαη		17 a l	Ual	ጥኒታዮ	Cor		λla	λla	Dro	Lvc		Thr	7 cn
254         Pro         Ala         Thr         Gly         Val         Leu         His         Lys         Ala         Cys         Leu         Lys         Pro         Ile         Gly         Ala         295         180 <td></td> <td>1111</td> <td>vai</td> <td>_</td> <td>пец</td> <td>Val</td> <td>Vai</td> <td>T Y T</td> <td></td> <td>116</td> <td>AΙα</td> <td>Αια</td> <td>110</td> <td>_</td> <td>AT 9</td> <td>1111</td> <td>ASP</td>		1111	vai	_	пец	Val	Vai	T Y T		116	AΙα	Αια	110	_	AT 9	1111	ASP
255       290       295       300         258       Thr Tyr Thr Asn Arg Thr Val Asn Thr Asp Lys Ala Glu Val Thr Asp 259 305       310       315       320         262       Val Ser Ile Glu Pro Ala Ser Pro Glu Glu Glu Ile Ala Asp Thr Val Lys 325       320       330       335       335         266       Val Met Gly Gly Glu Asp Trp Glu Leu Trp Ile Gln Ala Leu Ser Glu 340       345       350       350         270       Ala Gly Val Leu Ala Glu Gly Ala Lys Thr Val Ala Tyr Ser Tyr Ile 355       360       365       365         274       Gly Pro Glu Met Thr Trp Pro Val Tyr Trp Ser Gly Thr Ile Gly Glu 275       370       375       380       380         278       Ala Lys Lys Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr 385       390       395       400         282       Gly Cys Pro Ala Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala 283       405       415       415         286       Ser Ser Ala Ile Pro Val Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg 287       420       425       430         290       Val Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val 291       435       440       445         294       Arg Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val		Dro	λla		Clv	t/al	T.011	Hic		Δla	Cve	T.011	Lvc		т1Б	Glv	Δla
258       Thr       Tyr       Thr       Asn       Arg       Thr       Val       Asn       Thr       Asp       Lys       Ala       Glu       Thr       Asp       232       320       335       3		FIO		1111	Gry	vaı	пец		шуз	Ата	Cys	пец	_	110	110	Gry	AIG
259       305       310       315       320         262       Val Ser Ile Glu Pro Ala Ser Pro Glu Glu Ile Ala Asp Thr Val Lys       335       335       335         263       325       325       330       330       335         266       Val Met Gly Gly Glu Asp Trp Glu Leu Trp Ile Gln Ala Leu Ser Glu       360       345       350         270       Ala Gly Val Leu Ala Glu Gly Ala Lys Thr Val Ala Tyr Ser Tyr Ile       365       365         274       Gly Pro Glu Met Thr Trp Pro Val Tyr Trp Ser Gly Thr Ile Gly Glu       365         275       370       375       380         278       Ala Lys Lys Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr         279       385       390       395       400         282       Gly Cys Pro Ala Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala       410         283       405       410       410       415         286       Ser Ser Ala Ile Pro Val Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg       420       425       425       430         290       Val Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val       435       440       445         294       Arg Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val		Thr		Thr	Acn	Ara	Thr		Aen	Thr	Acn	Lvc		Glu	Val	Thr	Δen
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263       325       330       335       335       340       340       Asp Trp Glu Leu Trp Ile Gln Ala Leu Ser Glu 345       350       360       365			Ser	Tle	Glu	Pro		Ser	Pro	Glu	Glu		Δla	Asn	Thr	Val	
266 Val Met Gly Gly Glu Asp Trp Glu Leu Trp Ile Gln Ala Leu Ser Glu 340		• • • •	OC.		Olu		1114	001	110	OIU				11.00			270
267       340       345       350         270       Ala Gly Val Leu Ala Glu Gly Ala Lys Thr Val Ala Tyr Ser Tyr Ile         271       355       360       365         274       Gly Pro Glu Met Thr Trp Pro Val Tyr Trp Ser Gly Thr Ile Gly Glu       365         275       370       375       375       380         278       Ala Lys Lys Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr       390       395       400         282       Gly Cys Pro Ala Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala       405       415       415         286       Ser Ser Ala Ile Pro Val Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg       430       430         290       Val Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val       445         291       435       440       440       445         294       479       Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val		Val	Met	Glv	Glv		Asp	Trp	Glu	Leu		Tle	Gln	Δla	Leu		Glu
270 Ala Gly Val Leu Ala Glu Gly Ala Lys Thr Val Ala Tyr Ser Tyr Ile 271		•		017	_	014	1100	110				110	0111	1114		001	014
271		Ala	Glv	Val		Ala	G111	Glv			Thr	Val	Ala	Tvr		Tvr	Tle
274 Gly Pro Glu Met Thr Trp Pro Val Tyr Trp Ser Gly Thr Ile Gly Glu 375			<b>-</b> -1					V-1		-1-				_		-1-	
275       370       375       380         278       Ala Lys Lys Lys Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr         279       385       390       395       400         282       Gly Cys Pro Ala Tyr Pro Val Val Val Ala Lys Ala Leu Val Thr Gln Ala       415         283       405       410       415       415         286       Ser Ser Ala Ile Pro Val Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg       430       430         287       420       425       430       440         290       Val Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val       445         291       435       440       445       445         294       Arg Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val		Glv	Pro		Met	Thr	Trp	Pro		Tvr	Trp	Ser	Glv		Ile	Glv	Glu
278 Ala Lys Lys Asp Val Glu Lys Ala Ala Lys Arg Ile Thr Gln Gln Tyr 279 385		<b>0</b> -1								-1-	F		_			1	
279       385       390       395       400         282       Gly Cys       Pro Ala       Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala         283       405       410       410       415         286       Ser Ser Ala Ile Pro Val Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg       425       430         287       420       425       425       430         290       Val Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val       445         291       435       440       445       445         294       Arg Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val		Ala		Lvs	Asp	Val	Glu		Ala	Ala	Lvs	Ara		Thr	Gln	Gln	Tvr
282 Gly Cys Pro Ala Tyr Pro Val Val Ala Lys Ala Leu Val Thr Gln Ala 283			-,-		·p						-1-	-					
283			Cvs	Pro	Ala	Tvr		Val	Val	Ala	Lvs		Leu	Val	Thr	Gln	
286 Ser Ser Ala Ile Pro Val Val Pro Leu Tyr Ile Cys Leu Leu Tyr Arg 287		1	-1-			_					_						<del></del>
287 420 425 430  290 Val Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val  291 435 440 445  294 Arg Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val		Ser	Ser	Ala	Ile		Val	Val	Pro	Leu		Ile	Cvs	Leu	Leu		Ara
290 Val Met Lys Glu Lys Gly Thr His Glu Gly Cys Ile Glu Gln Met Val 291 435 440 445 294 Arg Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val											-1-		-1-			-1-	ر
291 435 440 445 294 Arg Leu Chr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val		Val	Met	Lvs		Lvs	Glv	Thr	His		Glv	Cvs	Ile	Glu		Met	Val
294 Arg Leu Leu Thr Thr Lys Leu Tyr Pro Glu Asn Gly Ala Pro Ile Val				_		-1-	1				1	-1-					<b>-</b>
		Ara	Leu		Thr	Thr	Lvs	Lev		Pro	Glu	Asn	Glv		Pro	Ile	Val
	295		450					455							-		

Input Set : F:\Final Sequence List-13987-00003-US.txt

Output Set: N:\CRF4\04262006\J574902.raw

298 Asp Glu Ala Gly Arg Val Arg Val Asp Asp Trp Glu Met Ala Glu Asp 299 465 470 475 302 Val Gln Gln Ala Val Lys Asp Leu Trp Ser Gln Val Ser Thr Ala Asn 485 490 306 Leu Lys Asp Ile Ser Asp Phe Ala Gly Tyr Gln Thr Glu Phe Leu Arg 500 505 310 Leu Phe Gly Phe Gly Ile Asp Gly Val Asp Tyr Asp Gln Pro Val Asp 515 520 314 Val Glu Ala Asp Leu Pro Ser Ala Ala Gln Gln 535 318 <210> SEQ ID NO: 3 319 <211> LENGTH: 837 320 <212> TYPE: DNA 321 <213> ORGANISM: Euglena gracilis 324 <400> SEQUENCE: 3 325 gggtggtata atacggtggc gttcgagaag gccgccctgg aggccgggct gtacgcccgg 60 327 ageettaatg gegaegeatt egaetetaea aegaaggege ggaeggttga ggegateaag 120 329 cgggateteg geaeggtgga cetegtggtg taeageateg eegeeeegaa aeggaeggae 180 331 cctgccaccg gcgtcgtcca caaggcctgc ctgaagccca tcggcgccac ctacaccaac 240 333 cqcactqtqa acaccqacaa ggcggagqtq accqatqtca gcatcqagcc ggcctccccc 300 335 gaggagateg cegacaeggt gaaggtgatg ggeggggagg actgggaget ttggateeag 360 337 gcactgtcgg aggccggcgt gctggcggag ggggccaaga cggtggcata ctcctacatc 420 339 ggccccgaga tgacgtggcc cgtgtactgg tccggcacca ttggggaggc caagaaggac 480 540 341 gtggagaagg ccgctaagcg catcacacag cagtacggct gcccagcata cccggtggtg 343 gecaaggeet tggtcaccca ggccagetet gecatecegg tggtgeeget etacatetge 600 345 ctgctgtacc gcgttatgaa ggagaagggc acccacgagg gctgcatcga gcagatggtg 660 347 eggetgetea ecaegaaget gtacceeggg aaeggtteee ecattgtega tgaggeeggg 720 780 349 cgggtgcggg tggatgactg ggagatggcg gaggatgtgc agcaggctgt gaaggacctc 351 tggagccagg tgaacactgc caacctcaag gacatttccg attttgccgg ctatgaa 837 354 <210> SEQ ID NO: 4 355 <211> LENGTH: 1329 356 <212> TYPE: DNA 357 <213> ORGANISM: Euglena gracilis 360 <220> FEATURE: 361 <221> NAME/KEY: CDS 362 <222> LOCATION: (1)..(1329) 365 <400> SEQUENCE: 4 366 atg ggc cgc cgc ggg gcc gca gtg ggc gcc gct cgt ggc cgc ggc 48 367 Met Gly Arg Arg Gly Ala Ala Val Gly Gly Ala Ala Arg Gly Arg Gly 10 96 370 ctc ctc cgc act ggc gct gtg gtg gtg aac atc gcc acc gcg gtc acc 371 Leu Leu Arg Thr Gly Ala Val Val Asn Ile Ala Thr Ala Val Thr 372 25 374 cac ctg gcc ccc ccg atg gcg atg ttc acc acc aca gcg aag gtc atc 144 375 His Leu Ala Pro Pro Met Ala Met Phe Thr Thr Ala Lys Val Ile 35 40 192 378 caq ccc aaq att cqt qqc ttc atc tqc acq acc acc cac ccq atc gqc

379 Gln Pro Lys Ile Arg Gly Phe Ile Cys Thr Thr His Pro Ile Gly

60

55

380

Input Set : F:\Final Sequence List-13987-00003-US.txt

Output Set: N:\CRF4\04262006\J574902.raw

## Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:12; N Pos. 3,15,18 Seq#:13; N Pos. 9,12

Seq#:26; Xaa Pos. 6,7,8,9

Seq#:29; Xaa Pos. 1,2

DATE: 04/26/2006 VERIFICATION SUMMARY PATENT APPLICATION: US/10/574,902 TIME: 07:34:05

Input Set : F:\Final Sequence List-13987-00003-US.txt

Output Set: N:\CRF4\04262006\J574902.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date L:1428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

L:1451 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0

L:1599 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:0

L:1638 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29 after pos.:0